SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

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<150> JP P2004-046238
<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac       96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
            20                  25                  30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg      144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
        35                  40                  45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac          189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
1               5                  10                  15

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac      96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
            20                  25                  30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg     144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
        35                  40                  45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac         189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
    50                  55                  60
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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1 5 10 15

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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1 5 10 15

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
50 55 60

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Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144

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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
        35                  40                  45

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac          189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
    50                  55                  60
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
        35                  40                  45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
    50                  55                  60
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Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
1               5                   10                  15

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac        96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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<213> Homo sapiens

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1 5 10 15

agg cgg gcg tcc cgc agt agc ggg cgg gcc cgg cgg ggg cgc cac gag 96
Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu

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                20                  25                  30

ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg      144
Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu
        35                  40                  45

gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg      192
Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala
    50                  55                  60

ctg cgg gcc ttt cgg ggt agc cgg tac ggg gac ttc aga cag atc cgg      240
Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg
65                  70                  75                  80

gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc      288
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
                85                  90                  95

gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tcg cgg att gaa gaa      336
Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
            100                 105                 110

ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gag ctc aca cca      384
Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro
        115                 120                 125

ctg gaa tca gct atc aat gtg ctg gag atg att aaa acg gaa ttt aca      432
Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr
    130                 135                 140

ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct      480
Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala
145                 150                 155                 160

gct gtc att att tgt atc aaa aac aaa gaa ttt gaa aag gct tca aaa      528
Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys
                165                 170                 175

att ttg aaa aaa cat atg tcc aag gac ccc aca act cag aag ctg aga      576
Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg
            180                 185                 190

aat gat ctc ctg aat att att cga gaa aag aac ttg gcc cat cct gtt      624
Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val
        195                 200                 205

atc cag aac ttt tca tat gag acc ttc cag cag aag atg ctg cgc ttc      672
Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe
    210                 215                 220

ctg gag agc cac ctg gat gac gcc gag ccc tac ctc ctc acg atg gcc      720
Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala
225                 230                 235                 240
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aaa aag gct ttg aaa tct gag tcc gct gcc tca agt aca ggg aag gaa      768
Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu
                245                 250                 255

gat aaa cag cca gca cca ggg cct gtg gaa aag cca ccc aga gaa ccc      816
Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro
            260                 265                 270

gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg      864
Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu
        275                 280                 285

aaa gca gct ttc aag act ctg tct ggt gca cag gat tct gag gca gcc      912
Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala
    290                 295                 300

ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc      960
Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu
305                 310                 315                 320

cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac     1008
Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn
                325                 330                 335

gaa agt tca gcc ccg gct gac ggt gag ggt ggc tcg gaa ctg cag ccc     1056
Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro
            340                 345                 350

aag aac aag cgc atg aca ata agc aga ttg gtc ttg gag gag gac agc     1104
Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser
        355                 360                 365

cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct     1152
Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala
    370                 375                 380

tca gcg cca cca tcc aag ccc acc gtt ctc aac caa ccc ctc cct gga     1200
Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly
385                 390                 395                 400

gag aag aat ccc aaa gta ccc aaa ggc aag tgg aac agc tct aat ggg     1248
Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly
                405                 410                 415

gtt gaa gaa aag gag act tgg gtg gaa gag gat gaa ctg ttt caa gtt     1296
Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val
            420                 425                 430

cag gca gca cca gat gaa gac agt aca acc aat ata aca aaa aag cag     1344
Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln
        435                 440                 445

aag tgg act gta gaa gaa agc gag tgg gtc aag gct gga gtg cag aaa     1392
Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys
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    450                 455                 460

tat ggg gaa gga aac tgg gct gcc att tct aaa aat tac cca ttt gtt      1440
Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val
465                 470                 475                 480

aac cga aca gct gtg atg att aag gat cgc tgg cgg acc atg aaa aga      1488
Asn Arg Thr Ala Val Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg
                485                 490                 495

ctt ggc atg aac                                                     1500
Leu Gly Met Asn
            500
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            20                  25                  30

Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu
        35                  40                  45

Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala
    50                  55                  60

Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg
65                  70                  75                  80

Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
                85                  90                  95

Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
            100                 105                 110

Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro
        115                 120                 125
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Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr
130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala
145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys
165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg
180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val
195 200 205

Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe
210 215 220

Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala
225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu
245 250 255

Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro
260 265 270

Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu
275 280 285

Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala
290 295 300

Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu
305 310 315 320

Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn
325 330 335

Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro
340 345 350

Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser
355 360 365

Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala
370 375 380

Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly
385 390 395 400

Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly
405 410 415

Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val
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Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln
435 440 445

Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys
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